

CDS: SPAC1F8.07c



WARNING: 30th July 2008

We continue to have problems downloading Boolean search results. We are working to resolve them.

Search for			Не			
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				Curato		
	General Informa	tion Add to Basket	₹∰ View Basket			
Systematic Name	SPAC1F8.07c					
Status	role inferred from homo	logy				
Product	pyruvate decarboxylase (predicted)					
Туре	CDS					
Sequence	DNA and Protein					
		Location				
Chromosome	1					
Contig Location	complement(10176010		* '			
Exons	complement(10176010	3544) (Spliced length:	1785 bp)			
Region download						
and display (in				Genome Browser		
Artemis)						
Context Map:						
	95000 100	105'000		.5'00		
SPNCRNA.139	SPAC1F8.04c isp3 fta5 :	SPAC1F8.07c< SPAC	1F8.08 SPAC11D3.01c	SPAC11D3.02c		
manda amuningan		D3.03c SPAC11D3.04c				
		Curation				
Term			Other genes annotated			
conserved protein similar to S. pombe SPAC186.09 (paralog)			(81 Others) (0 Others)			
similar to S. pombe S	PAC180.09 (paralog)		(0 Otners	,		
	Prec	licted Peptide Properti	es			
	64.7 kDa	Amino acids	594			
Mass	04.7 KDa					
	pH 5.9	Charge	-4.5			
Isoelectric point						
Isoelectric point Signal Peptide Transmembrane	pH 5.9					
Isoelectric point Signal Peptide	pH 5.9 Not found					

Term (browse	: Amigo)	Qualifier	Evidence	Other genes annotated to this term		
Biological F	rocess					
generation of precursor metabolites and energy		metabolites	NAS	120 others		
		ess	ISS (PMID:17072883) with Interpro:IPR012110	25 others		
Molecular l	Function					
			IEA (GOA:interprolGO_REF:0000002) with InterPro:IPR000399	89 others		
pyruvate decarboxylase activity		activity	ISS (PMID:17072883) with Interpro:IPR012110	3 others		
			IEA (GOA:interprolGO_REF:0000002) with InterPro:IPR000399	6 others		
			IEA (GOA:interprolGO_REF:0000002) with InterPro:IPR000399	645 others		
			Catalytic Activity			
EC 4.1.1.1:	IUBMB					
		P	ublished Expression Profiles			
Gene Expres	sion Viewer	Cell Cycle Meiosi	Environmental Stress Pheromone Response/Mating			
Transcripton	neViewer	SPAC1F8.07c Hig	h-resolution view of transcripts in neighbourhood			
			Literature			
Search for in	PubMed					
			Domain Information			
		ture for this gene pro	oduct			
View SCOP	superfamily					
DB	Accs	Description				
Pfam	PF02776	Thiamine pyrophosphate enzyme, N-terminal TPP binding domain				
Pfam	PF00205	Thiamine pyrophosphate enzyme, central domain				
Pfam	PF02775 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain					
InterPro IPR012110 Pyruvate decarboxylase/indolepyruvate decarboxylase						
InterPro IPR000399 TPP-binding enzymes						
InterPro	15 1 1					
InterPro IPR011766 Thiamine pyrophosphate enzyme, C-terminal TPP-binding						
InterPro						
PROSITE	PS00187	Thiamine pyrophosi	phate enzymes signature.			
		1	Database Cross-References			
DB	Accs	Description				
UniProtKB	Q92345	Probable pyruva	te decarboxylase C1F8.07c (EC 4.1.1.1).			
EMBL	CU329670 Schizosaccharomyces pombe chromosome I					
Biotwiki	SPAC1F8_07c Biotwiki					
NCBI Entrez Gene SPAC1F8.07c NCBI Entrez Gene						

FYSSION SPAC1F8.07c FYSSION GermOnline SPAC1F8.07c GermOnline NBRP SPAC1F8.07c Fission yeast strain database, National BioResource Project (Japan)

PIR T38114 PIR

YOGY SPAC1F8.07c Retrieval of eukaryotic orthologs

UniProtKB Annotation For This Protein

Catalytic Activity A 2-oxo acid = an aldehyde + CO(2).

Cofactor Binds 1 metal ion per subunit.; Binds 1 thiamine pyrophosphate per subunit.

Similarity Belongs to the TPP enzyme family.

Subunit Homotetramer (By similarity).

Complete proteome (4982 others), Decarboxylase (11 others), Flavoprotein (45 others), Keywords

Lyase (60 others), Magnesium (81 others), Metal-binding (451 others), Thiamine

pyrophosphate (11 others)

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Curator feedback

Technical feedback